

CLAIMS

- 1 Method for characterizing the state of a neoplastic disease in a subject, comprising
- 5 (i) determining the pattern of expression levels of at least 6, 8, 10, 15, 20, 30, or 47 marker genes, comprised in a group of marker genes consisting of SEQ ID NO:1 to 165, in a biological sample from said subject,
- (ii) comparing the pattern of expression levels determined in (i) with one or several reference pattern(s) of expression levels,
- (iii) characterizing the state of said neoplastic disease in said subject from the outcome of the comparison in step (ii).
- 10 2 Method for characterizing the state of a neoplastic disease in a subject, comprising
- (i) determining the pattern of expression levels of at least 6, 8, 10, 15, 20, 30, 47 or 67 marker genes, comprised in a group of marker genes consisting of SEQ ID NO:1 to 165 and 472 to 491, in a biological sample from said subject,
- 15 (ii) comparing the pattern of expression levels determined in (i) with one or several reference pattern(s) of expression levels,
- (iii) characterizing the state of said neoplastic disease in said subject from the outcome of the comparison in step (ii).
- 3 Method for detection, diagnosis, screening, monitoring, and/or prognosis of a neoplastic disease in a subject, comprising
- 20 (i) determining the pattern of expression levels of at least 1, 2, 3, 5, 10, 15, 20, 30, or 47 marker genes, comprised in a group of marker genes consisting of SEQ ID NOs:1 to 17, 19 to 33, 35 to 50, 52 to 64, 66 to 85, 88 to 91, and 93 to 165 in biological samples from said subject,
- 25 (ii) comparing the pattern of expression levels determined in (i) with one or several reference pattern(s) of expression levels,
- (iii) detecting, diagnosing, screening, monitoring, and/or prognosing said neoplastic disease in said subject from the outcome of the comparison in step (ii).

- 4 Method for detection, diagnosis, screening, monitoring, and/or prognosis of a neoplastic disease in a subject, comprising
- 5 (i) determining the pattern of expression levels of at least 1, 2, 3, 5, 10, 15, 20, 30, 47, or 67 marker genes, comprised in a group of marker genes consisting of SEQ ID NOs:1 to 17, 19 to 33, 35 to 50, 52 to 64, 66 to 85, 88 to 91, and 93 to 165 and 472 to 491 in biological samples from said subject,
- 10 (ii) comparing the pattern of expression levels determined in (i) with one or several reference pattern(s) of expression levels,
- (iii) detecting, diagnosing, screening, monitoring, and/or prognosing said neoplastic disease in said subject from the outcome of the comparison in step (ii).
- 5 Method of any of claims 1 to 4, wherein said method comprises multiple determinations of a pattern of expression levels, at different points in time, thereby allowing to monitor the development of said neoplastic disease in said subject.
- 15 6 Method of claim 1 or 2, wherein said method comprises an estimation of the likelihood of success of a given mode of treatment for said neoplastic disease in said subject.
- 7 Method of claim 1 or 2, wherein said method comprises an assessment of whether or not the subject is expected to respond to a given mode of treatment for said neoplastic disease.
- 8 Method of claim 6 or 7, wherein a predictive algorithm is used.
- 9 Method of claim 8, wherein the predictive algorithm is a Support Vector Machine.
- 20 10 Method of any of claims 6 to 9, wherein said given mode of treatment
- (i) acts on cell proliferation, and/or
- (ii) acts on cell survival, and/or
- (iii) acts on cell motility, and/or
- (iv) is an anthracycline based mode of treatment, and/or
- 25 (v) comprises administration of epirubicin and/or cyclophosphamid.
- 11 Method of treatment for a subject afflicted with a neoplastic disease, comprising

- (i) identifying the most promising mode of treatment with the method of claim 6 or 7,
- (ii) treating said neoplastic disease in said patient by the mode of treatment identified in step (i).

12 Method of screening for subjects afflicted with a neoplastic disease, wherein a method of
5 any of claims 1 to 4 is applied to a plurality of subjects.

13 Method of screening for substances and/or therapy modalities having curative effect on a
neoplastic disease comprising

- (i) obtaining a biological sample from a subject afflicted with said neoplastic disease,
- (ii) assessing, from said biological sample, using the method of claim 6 or 7, whether
10 said subject is expected to respond to a given mode of treatment for said neoplastic
disease,
- (iii) if said subject is expected to respond to said given mode of treatment, incubating
said biological sample with said substance under said therapy modalities,
- (iv) observing changes in said biological sample triggered by said test substance under
15 said therapy modalities,
- (v) selecting or rejecting said test substance and/or said therapy modalities, based on
the observation of changes in said biological sample under (iv).

14 Method of screening for compounds having curative effect on a neoplastic disease
comprising

- (i) incubating biological samples or extracts of these with a test substance,
- (ii) determining the pattern of expression levels of at least 1, 2, 3, 5, 10, 15, 20, 30, or
47 marker genes, comprised in a group of marker genes consisting of SEQ ID
NO:1 to 17, 19 to 33, 35 to 50, 52 to 64, 66 to 85, 88 to 91, and 93 to 165 in said
biological sample,
- (iii) comparing the pattern of expression levels determined in (ii) with one or several
reference pattern(s),
25
- (iv) selecting or rejecting said test substance, based on the comparison performed
under (iii).

- 15 Method of screening for compounds having curative effect on a neoplastic disease comprising
- 5 (i) incubating biological samples or extracts of these with a test substance,
- (ii) determining the pattern of expression levels of at least 1, 2, 3, 5, 10, 15, 20, 30, 47, or 67 marker genes, comprised in a group of marker genes consisting of SEQ ID NO:1 to 17, 19 to 33, 35 to 50, 52 to 64, 66 to 85, 88 to 91, and 93 to 165 and 472 to 491 in said biological sample,
- (iii) comparing the pattern of expression levels determined in (ii) with one or several reference pattern(s),
- 10 (iv) selecting or rejecting said test substance, based on the comparison performed under (iii).
- 16 Method of any of claims 1 to 15 wherein said marker genes are comprised in a group of marker genes listed in Table 2.
- 17 Method of any of claims 1 to 16, wherein the expression level is determined
- 15 (i) with a hybridization based method, or
- (ii) with a hybridization based method utilizing arrayed probes, or
- (iii) with a hybridization based method utilizing individually labeled probes, or
- (iv) by real time real time PCR, or
- (v) by assessing the expression of polypeptides, proteins or derivatives thereof, or
- 20 (vi) by assessing the amount of polypeptides, proteins or derivatives thereof.
- 18 Method of any of claims 1 to 17, wherein the neoplastic disease is breast cancer.
- 19 A kit comprising at least 6, 8, 10, 15, 20, 30, or 47 primer pairs and probes suitable for marker genes comprised in a group of marker genes consisting of
- (i) SEQ ID NO:1 to SEQ ID NO:165, or
- 25 (iii) the marker genes listed in Table 2.

- 20 A kit comprising at least 6, 8, 10, 15, 20, 30, 47, or 67 primer pairs and probes suitable for marker genes comprised in a group of marker genes consisting of
- (i) SEQ ID NO:1 to SEQ ID NO:165, and/or
- (ii) SEQ ID NO:472 to SEQ ID NO:491, or
- 5 (iii) the marker genes listed in Table 2.
- 21 A kit comprising at least 6, 8, 10, 15, 20, 30, or 47 individually labeled probes, each having a sequence comprised in a group of sequences consisting of SEQ ID NO:331 to SEQ ID NO:471.
- 22 A kit comprising at least 6, 8, 10, 15, 20, 30, 47 or 67 individually labeled probes, each
10 having a sequence comprised in a group of sequences consisting of SEQ ID NO:331 to SEQ ID NO:471 and SEQ ID NO:512 to 571.
- 23 A kit comprising at least 6, 8, 10, 15, 20, 30, or 47 arrayed probes, each having a sequence comprised in a group of sequences consisting of SEQ ID NO:331 to SEQ ID NO:471.
- 24 A kit comprising at least 6, 8, 10, 15, 20, 30, 47 or 67 arrayed probes, each having a
15 sequence comprised in a group of sequences consisting of SEQ ID NO:331 to SEQ ID NO:471 and SEQ ID NO:512 to 571.